

SEQUENCE LISTING

<110> YUE, Henry
 LAL, Preeti
 TANG, Y. Tom
 LU, Dyung Aina M.
 AU-YOUNG, Janice

<120> MITOCHONDRIAL PROTEINS

<130> PF-0678 US

<140> To Be Assigned

<141> Herewith

<150> 60/124,655

<151> 1999-03-16

<160> 16

<170> PERL Program

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<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1676225CD1

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Gly	Leu	Arg	Ser	Ser	Val	Gly	Pro	Ala	Val	Gln	Ala	Arg	Gly	Val	20	25	30	35
His	Gln	Ser	Val	Ala	Thr	Asp	Gly	Pro	Ser	Ser	Thr	Gln	Pro	Ala	40	45	50	55
Leu	Pro	Lys	Ala	Arg	Ala	Val	Ala	Pro	Lys	Pro	Ser	Ser	Arg	Gly	60	65	70	75
Glu	Tyr	Val	Val	Ala	Lys	Leu	Asp	Asp	Leu	Val	Asn	Trp	Ala	Arg	80	85	90	95
Arg	Ser	Ser	Leu	Trp	Pro	Met	Thr	Phe	Gly	Leu	Ala	Cys	Cys	Ala	100	105	110	115
Val	Glu	Met	Met	His	Met	Ala	Ala	Pro	Arg	Tyr	Asp	Met	Asp	Arg	120	125	130	135
Phe	Gly	Val	Val	Phe	Arg	Ala	Ser	Pro	Arg	Gln	Ser	Asp	Val	Met	140	145	150	155
Ile	Val	Ala	Gly	Thr	Leu	Thr	Asn	Lys	Met	Ala	Pro	Ala	Leu	Arg	160	165	170	175
Lys	Val	Tyr	Asp	Gln	Met	Pro	Glu	Pro	Arg	Tyr	Val	Val	Ser	Met	180	185	190	195
Gly	Ser	Cys	Ala	Asn	Gly	Gly	Gly	Tyr	Tyr	His	Tyr	Ser	Tyr	Ser	200	205	210	
Val	Val	Arg	Gly	Cys	Asp	Arg	Ile	Val	Pro	Val	Asp	Ile	Tyr	Ile				
Pro	Gly	Cys	Pro	Pro	Thr	Ala	Glu	Ala	Leu	Leu	Tyr	Gly	Ile	Leu				
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Tyr	Arg	Arg																

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Ile	Leu	Ser	Gln	Pro	Leu	Met	Tyr	Val	Lys	Val	Leu	Ile	Gln	Val
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Gly	Tyr	Glu	Pro	Leu	Pro	Pro	Thr	Ile	Gly	Arg	Asn	Ile	Phe	Gly
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Arg	Gln	Val	Cys	Gln	Leu	Pro	Gly	Leu	Phe	Ser	Tyr	Ala	Gln	His
				50					55					60
Ile	Ala	Ser	Ile	Asp	Gly	Arg	Arg	Gly	Leu	Phe	Thr	Gly	Leu	Thr
				65					70					75
Pro	Arg	Leu	Cys	Ser	Gly	Val	Leu	Gly	Thr	Val	Val	His	Gly	Lys
				80					85					90
Val	Leu	Gln	His	Tyr	Gln	Glu	Ser	Asp	Lys	Gly	Glu	Glu	Leu	Gly
				95					100					105
Pro	Gly	Asn	Val	Gln	Lys	Glu	Val	Ser	Ser	Ser	Phe	Asp	His	Val
				110					115					120
Ile	Lys	Glu	Thr	Thr	Arg	Glu	Met	Ile	Ala	Arg	Ser	Ala	Ala	Thr
				125					130					135
Leu	Ile	Thr	His	Pro	Phe	His	Val	Ile	Thr	Leu	Arg	Ser	Met	Val
				140					145					150
Gln	Phe	Ile	Gly	Arg	Glu	Ser	Lys	Tyr	Cys	Gly	Leu	Cys	Asp	Ser
				155					160					165
Ile	Ile	Thr	Ile	Tyr	Arg	Glu	Glu	Gly	Ile	Leu	Gly	Phe	Phe	Ala
				170					175					180
Gly	Leu	Val	Pro	Arg	Leu	Leu	Gly	Asp	Ile	Leu	Ser	Leu	Trp	Leu
				185					190					195
Cys	Asn	Ser	Leu	Ala	Tyr	Leu	Val	Asn	Thr	Tyr	Ala	Leu	Asp	Ser
				200					205					210
Gly	Val	Ser	Thr	Met	Asn	Glu	Met	Lys	Ser	Tyr	Ser	Gln	Ala	Val
				215					220					225
Thr	Gly	Phe	Phe	Ala	Ser	Met	Leu	Thr	Tyr	Pro	Phe	Val	Leu	Val
				230					235					240
Ser	Asn	Leu	Met	Ala	Val	Asn	Asn	Cys	Gly	Leu	Ala	Gly	Gly	Cys
				245					250					255
Pro	Pro	Tyr	Ser	Pro	Ile	Tyr	Thr	Ser	Trp	Ile	Asp	Cys	Trp	Cys
				260					265					270
Met	Leu	Gln	Lys	Glu	Gly	Asn	Met	Ser	Arg	Gly	Asn	Ser	Leu	Phe
				275					280					285
Phe	Arg	Lys	Val	Ala	Phe	Gly	Lys	Thr	Tyr	Cys	Cys	Asp	Leu	Lys
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Met	Leu	Ile												

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Asn	Ser	Asp	Val	Asn	Asn	Leu	Met	Ala	Val	Leu	Asn	Met	Ser	Asn
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Met	Leu	Pro	Glu	Gly	Leu	Phe	Pro	Glu	His	Leu	Ile	Asp	Val	Leu
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3

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Gln	Val	Thr	Glu	Ser	Val	Ser	Asp	Ser	Ile	Thr	Val	Leu	Pro	
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Asp	Lys	Lys	Lys	Phe	Tyr	Val	Phe	Gly	Val	Ala	Met	Thr	Met	Met
				20					25					30
Ile	Arg	Val	Ser	Val	Tyr	Pro	Phe	Thr	Leu	Ile	Arg	Thr	Arg	Leu
				35					40					45
Gln	Val	Gln	Lys	Gly	Lys	Ser	Leu	Tyr	His	Gly	Thr	Phe	Asp	Ala
				50					55					60
Phe	Ile	Lys	Ile	Leu	Arg	Ala	Asp	Gly	Ile	Thr	Gly	Leu	Tyr	Arg
				65					70					75
Gly	Phe	Leu	Val	Asn	Thr	Phe	Thr	Leu	Ile	Ser	Gly	Gln	Cys	Tyr
				80					85					90
Val	Thr	Thr	Tyr	Glu	Leu	Thr	Arg	Lys	Phe	Val	Ala	Asp	Tyr	Ser
				95					100					105
Gln	Ser	Asn	Thr	Val	Lys	Ser	Leu	Val	Ala	Gly	Gly	Ser	Ala	Ser
				110					115					120
Leu	Val	Ala	Gln	Ser	Ile	Thr	Val	Pro	Ile	Asp	Val	Val	Ser	Gln
				125					130					135
His	Leu	Met	Met	Gln	Arg	Lys	Gly	Glu	Lys	Met	Gly	Arg	Phe	Gln
				140					145					150
Val	Arg	Gly	Asn	Ser	Glu	Gly	Gln	Gly	Val	Val	Ala	Phe	Gly	Gln
				155					160					165
Thr	Lys	Asp	Ile	Ile	Arg	Gln	Ile	Leu	Gln	Ala	Asp	Gly	Leu	Arg
				170					175					180
Gly	Phe	Tyr	Arg	Gly	Tyr	Val	Ala	Ser	Leu	Leu	Thr	Tyr	Ile	Pro
				185					190					195
Asn	Ser	Ala	Val	Trp	Trp	Pro	Phe	Tyr	His	Phe	Tyr	Ala	Glu	Gln
				200					205					210
Leu	Ser	Tyr	Leu	Cys	Pro	Lys	Glu	Cys	Pro	His	Ile	Val	Phe	Gln
				215					220					225
Ala	Val	Ser	Gly	Pro	Leu	Ala	Ala	Ala	Thr	Ala	Ser	Ile	Leu	Thr
				230					235					240
Asn	Pro	Met	Asp	Val	Ile	Arg	Thr	Arg	Val	Gln	Val	Glu	Gly	Lys
				245					250					255
Asn	Ser	Ile	Ile	Leu	Thr	Phe	Arg	Gln	Leu	Met	Ala	Glu	Glu	Gly
				260					265					270
Pro	Trp	Gly	Leu	Met	Lys	Gly	Leu	Ser	Ala	Arg	Ile	Ile	Ser	Ala
				275					280					285
Thr	Pro	Ser	Thr	Ile	Val	Ile	Val	Val	Gly	Tyr	Glu	Ser	Leu	Lys
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Lys	Leu	Ser	Leu	Arg	Pro	Glu	Leu	Val	Asp	Ser	Arg	His	Trp	
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Leu	Gly	Gln	Thr	Val	Gly	Trp	Pro	Cys	Gly	Ala	Leu	Gly	Pro	Gly
				20					25					30
Pro	His	Arg	Trp	Gly	Pro	Cys	Gly	Gly	Ser	Trp	Ala	Gln	Lys	Phe
				35					40					45
Tyr	Gln	Asp	Gly	Pro	Gly	Arg	Gly	Leu	Gly	Glu	Glu	Asp	Ile	Arg
				50					55					60
Arg	Ala	Arg	Glu	Ala	Arg	Pro	Arg	Lys	Thr	Pro	Arg	Pro	Gln	Leu
				65					70					75
Ser	Asp	Arg	Ser	Arg	Glu	Arg	Lys	Val	Pro	Ala	Ser	Arg	Ile	Ser
				80					85					90
Arg	Leu	Ala	Asn	Phe	Gly	Gly	Leu	Ala	Val	Gly	Leu	Gly	Leu	Gly
				95					100					105
Val	Leu	Ala	Glu	Met	Ala	Lys	Lys	Ser	Met	Pro	Gly	Gly	Arg	Leu
				110					115					120
Gln	Ser	Glu	Gly	Gly	Ser	Gly	Leu	Asp	Ser	Ser	Pro	Phe	Leu	Ser
				125					130					135
Glu	Ala	Asn	Ala	Glu	Arg	Ile	Val	Gln	Thr	Leu	Cys	Thr	Val	Arg
				140					145					150
Gly	Ala	Ala	Leu	Lys	Val	Gly	Gln	Met	Leu	Ser	Ile	Gln	Asp	Asn
				155					160					165
Ser	Phe	Ile	Ser	Pro	Gln	Leu	Gln	His	Ile	Phe	Glu	Arg	Val	Arg
				170					175					180
Gln	Ser	Ala	Asp	Phe	Met	Pro	Arg	Trp	Gln	Met	Leu	Arg	Val	Leu
				185					190					195
Glu	Glu	Glu	Leu	Gly	Arg	Asp	Trp	Gln	Ala	Lys	Val	Ala	Ser	Leu
				200					205					210
Glu	Glu	Val	Pro	Phe	Ala	Ala	Ala	Ser	Ile	Gly	Gln	Val	His	Gln
				215					220					225
Gly	Leu	Leu	Arg	Asp	Gly	Thr	Glu	Val	Ala	Val	Lys	Ile	Gln	Tyr
				230					235					240
Pro	Gly	Ile	Ala	Gln	Ser	Ile	Gln	Ser	Asp	Val	Gln	Asn	Leu	Leu
				245					250					255
Ala	Val	Leu	Lys	Met	Ser	Ala	Ala	Leu	Pro	Ala	Gly	Leu	Phe	Ala
				260					265					270
Glu	Gln	Ser	Leu	Gln	Ala	Leu	Gln	Gln	Glu	Leu	Ala	Trp	Glu	Cys
				275					280					285
Asp	Tyr	Arg	Arg	Glu	Ala	Ala	Cys	Ala	Gln	Asn	Phe	Arg	Gln	Leu
				290					295					300
Leu	Ala	Asn	Asp	Pro	Phe	Phe	Arg	Val	Pro	Ala	Val	Val	Lys	Glu
				305					310					315
Leu	Cys	Thr	Thr	Arg	Val	Leu	Gly	Met	Glu	Leu	Ala	Gly	Gly	Val
				320					325					330
Pro	Leu	Asp	Gln	Cys	Gln	Gly	Leu	Ser	Gln	Asp	Leu	Arg	Asn	Gln
				335					340					345
Ile	Cys	Phe	Gln	Leu	Leu	Thr	Leu	Cys	Leu	Arg	Glu	Leu	Phe	Glu
				350					355					360
Phe	Arg	Phe	Met	Gln	Thr	Asp	Pro	Asn	Trp	Ala	Asn	Phe	Leu	Tyr
				365					370					375
Asp	Ala	Ser	Ser	His	Gln	Val	Thr	Leu	Leu	Asp	Phe	Gly	Ala	Ser
				380					385					390
Arg	Glu	Phe	Gly	Thr	Glu	Phe	Thr	Asp	His	Tyr	Ile	Glu	Val	Val
				395					400					405
Lys	Ala	Ala	Ala	Asp	Gly	Asp	Arg	Asp	Cys	Val	Leu	Gln	Lys	Ser
				410					415					420
Arg	Asp	Leu	Lys	Phe	Leu	Thr	Gly	Phe	Glu	Thr	Lys	Ala	Phe	Ser
				425					430					435
Asp	Ala	His	Val	Glu	Ala	Val	Met	Ile	Leu	Gly	Glu	Pro	Phe	Ala
				440					445					450
Thr	Gln	Gly	Pro	Tyr	Asp	Phe	Gly	Ser	Gly	Glu	Thr	Ala	Arg	Arg
				455					460					465

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Ile	Gln	Asp	Leu	Ile	Pro	Val	Leu	Leu	Arg	His	Arg	Leu	Cys	Pro
				470					475					480
Pro	Pro	Glu	Glu	Thr	Tyr	Ala	Leu	His	Arg	Lys	Leu	Ala	Gly	Ala
				485					490					495
Phe	Leu	Ala	Cys	Ala	His	Leu	Arg	Ala	His	Ile	Ala	Cys	Arg	Asp
				500					505					510
Leu	Phe	Gln	Asp	Thr	Tyr	His	Arg	Tyr	Trp	Ala	Ser	Arg	Gln	Pro
				515					520					525
Asp	Ala	Ala	Thr	Ala	Gly	Ser	Leu	Pro	Thr	Lys	Gly	Asp	Ser	Trp
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Val	Asp	Pro	Ser											

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				20					25					30
Val	Cys	Ser	Lys	Lys	Lys	Ile	Lys	Thr	Asp	Lys	Pro	Tyr	Gly	Ile
				35					40					45
Gly	Gly	Gly	Leu	Thr	Val	Asp	Val	Asp	Ala	Asn	Gly	Arg	Lys	Gly
				50					55					60
Lys	Gly	Lys	Gly	Val	Tyr	Gln	Phe	Val	Asp	Lys	Tyr	Gly	Ala	Asn
				65					70					75
Val	Asp	Gly	Tyr	Ser	Pro	Ile	Tyr	Asn	Glu	Asp	Asp	Trp	Ser	Pro
				80					85					90
Thr	Gly	Asp	Val	Tyr	Val	Gly	Gly	Thr	Thr	Gly	Leu	Leu	Ile	Trp
				95					100					105
Ala	Val	Thr	Leu	Ala	Gly	Ile	Leu	Gly	Gly	Gly	Ala	Leu	Leu	Val
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Tyr	Asn	Thr	Ser	Ala	Leu	Ser	Gly							
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				20					25					30
Thr	Thr	Lys	Ile	His	His	Lys	Val	Thr	Glu	Asn	Trp	Ile	Ser	Ala
				35					40					45
Thr	Leu	Leu	Leu	Thr	Pro	Val	Val	Gly	Thr	Tyr	Gln	Tyr	Ala	Met
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 atatgagccg aggaaatagc ttatttttcc ggaaggtcgc ctttggaag acttattgtt 960
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<210> 12
<211> 741
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 3126833CB1

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<210> 13
<211> 1759
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> Incyte ID No: 3446038CB1

<400> 13


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<210> 14
 <211> 2188
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 4113161CB1

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<210> 15
 <211> 488
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 4408678CB1

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<400> 15
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<210> 16
 <211> 473
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 4942111CB1

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atccaccaca aggtcaccga gaactggatc tccgccacgc tcctcctcac ccccgctcgtc 180
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